

## **SEQUENCE LISTING**

<110> Jayashree Aiyar  
Claudia Ann Iannotti  
Edward Philip Christian  
Naomi Jean Logsdon

<120> HUMAN BRAIN-DERIVED TISSUE-SPECIFIC POTASSIUM CHANNEL

<130> PHM.70293

<150> GB 9726339.6  
<151> 1997-12-13

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1  
<211> 3029  
<212> DNA  
<213> Homo sapiens

<400> 1

gccaggcacc atgggtcaga agtcgcgcaa cggcgccgta taccccgccc	cgagcgggga	60
gaagaagctg aagggtggct tcgtgggct ggaccccgcc gcccggact	ccacccggga	120
cggggcgctg ctgatcgccg gctccgaggc ccccaagcgc ggcagcatcc	tcagcaaacc	180
tgcgcgggct ggcgcggcg cgggaagcc ccccaagcgc aacgccttct	accgcaagct	240
gcagaatttc ctctacaacg tgctggagcg gccgcgcggc tggcgttca	tctaccacgc	300
ctacgtgttc ctccctggtt tctccctgcct cgtgctgtct gtgtttcca	ccatcaagga	360
gtatgagaag agctcggagg gggccctcta catcctggaa atcgtgacta	tcgtgggtt	420
ttgcgtggag tacttcgtgc ggatctggc cgcaggctgc tgctgcccgt	accgtggctg	480
gaggggggcggt ctaaagtggc cccggaaacc gttctgtgt attgacatca	tggtgctcat	540
cgcctccatt ggggtgctgg ccgcggccct ccaggcaac gtcttgcca	catctgcgct	600
ccggaggctg cgcttctgc agattctgcg gatgatccgc atggaccggc	ggggaggcac	660
ctggaaagctg ctgggtctgtc tggttatgc ocacagcaag gagetggtca	ctgccttgta	720
catcggcttc ctttgtctca tcctggcctc gttcctgggt tacttggcag	agaaggggga	780
gaacgaccac ttgacacact acgcggatgc actctggtgg ggcctgatca	cgctgacacc	840
attggctacg gggacaagta ccccaagacc tggAACGGCA ggctccttgc	ggcaaccttc	900
accctcatcg gtgtctcctt ctgcggctg cctgcaggca tcttgggtc	tgggttgcc	960
ctgaagggttc aggagcagca caggcagaag cacttggaga agaggcgaa	cccgccagca	1020
ggcctgatcc agtccggctg gagattctac gccaccaacc tctcgccac	agacctgcac	1080
tccacgtggc agtactacga gcgaacggtc accgtgcca tgtacagttc	gcaaactcaa	1140
acctacgggg cctccagact tatccccccg ctgaaccagc tggagctgct	gaggaacctc	1200
aagagtaaat ctggactcgc tttcaggaag gaccccccgc cggagccgtc	tccaagccag	1260
aaggctcgtt taaaagatcg tgtcttctcc agcccccgag gctggctgc	caaggggaaag	1320
gggtccccgc aggcccagac tgtgaggcgg tcaccagcg ccgaccagag	cctcgaggac	1380
agccccagca aggtgccccaa gagctggagc ttccgggacc gcagccggc	acgcccaggct	1440
ttccgcatca agggtgccgc gtcacggcag aactcagaag aagcaagct	ccccggagag	1500
gacattgtgg atgacaagag ctgcccctgc gagttgtga ccgaggac	gacccgggac	1560
ctcaaagtca gcatcagagc cgtgtgtgtc atgcggttcc tgggttccaa	gcggaagttc	1620
aggagagacc tggggcccta cgacgtgtat gacgtcatcg agcagtactc	agccggccac	1680
ctggacatgc tggccgaat taagagctg cagtcagag tggaccat	cgtggggcgg	1740
ggcccagcga tcacggacaa ggacccgacc aagggccccc cggaggcgg	gctcccgag	1800
gaccccgacca tggatggac gtcgggaag gtggagaac aggtttgtc	catggagaag	1860
aagctggact tcttggatata ttttccatcg cagccgtatgg gatcccccc	gacagagacc	1920
gaggcctat tggggcccaa agagccggag ccggccccc cgttaccacag	ccccggagac	1980
agccggggac atgtcgacag gcacggctgc attgtcaaga tcgtgcgtc	cagcagttcc	2040
acggggccaga agaacttctc ggccggcccg gcccgcggcc ctgtccatgt	tccgcctcc	2100
acctcctggc agccacagag ccacccggc cagggccacg gcacccccc	cgtggggac	2160
cacggctccc tggtgcgtat cccggcccg cttgtccacg agcggtcgct	gtccgcctac	2220
ggcgggggca acccgccag catggatcc ctgcggcagg aggacacccc	gggctgcagg	2280
ccccccgagg ggacccctgcg ggacagcgac acgtccatct ccatccgc	cgtggaccac	2340
gaggagctgg agcggtctt cagcggcttc agcatctccc agtccaagga	gaacctggat	2400
gctctcaaca gctgtacgc ggccgtggcg cttgtgcca aagtcaaggcc	ctacattgcg	2460

gaggagaggt	cagacaccga	ctccgacctc	tgtacccgt	gcggggcccc	gccacgctcg	2520
gccaccggcg	agggtccctt	tggtgacgtg	ggctggccg	ggcccaggaa	gtgaggcggc	2580
gctggccag	tggacccgcc	cgcggccctc	ctcagcacgg	tgcctccgag	gttttgaggc	2640
ggaaacctc	tggggccctt	ttcttacagt	aactgagtgt	ggcgggaagg	gtgggcccctg	2700
gaggggcca	tgtgggctga	aggatggggg	ctcctggcag	tgacccttta	caaaagttat	2760
tttccaacag	gggctggagg	gctgggcagg	gccctgtggc	tccaggagca	gcgtgcagga	2820
gcaaggctgc	cctgtccact	ctgctcaggg	ccgcggccga	catcagcccg	gtgtgaggag	2880
gggcgggagt	gatgacgggg	tgttgccagc	gtggcaacag	gcgggggtt	gtctcagccg	2940
agcccagggg	aggcacaaaag	ggcaggctg	ttccctgagg	acctgcgcaa	agggcgggcc	3000
tgtttggtga	ggacctgcgg	ccttgggtc				3029

<210> 2  
<211> 2565  
<212> DNA  
<213> Homo sapiens

<400> 2						
atggtcaga	agtgcgccaa	cggccgcgt	tacccggcc	cgagcgggg	gaagaagctg	60
aagggtggct	tcgtggggct	ggacccggc	gcgcggcact	ccacccgg	cggggcgctg	120
ctgatcgccg	gctccgaggc	ccccaa	ggcagcatcc	tcagcaaa	tcgcgcggc	180
ggcgcggcg	ccggaaagcc	ccccaa	aacgcctt	accgaagct	gcagaatttc	240
ctctacaacg	tgctggagcg	gccgcgcgc	tggcggttca	tctaccacgc	ctacgtttc	300
ctcctgggtt	tctctgcct	cgtgctgtct	gtgtttcca	ccatcaagga	gtatgagaag	360
agctcggagg	ggccctcta	catcctggaa	atcgtgacta	tcgtgggtt	tggcgtggag	420
tacttcgtgc	ggatctggc	cgcaggctgc	tgctgcccgt	accgtggctg	gagggggcgg	480
ctcaagttt	cccgaaacc	gttctgtgt	attgacatca	tgggtctcat	ccgcctccatt	540
gcgggtgtgg	ccggccgctc	ccaggcAAC	gtctttgc	catctgcgt	ccggagcctg	600
cgcttccgtc	agatttcgtc	gatgatccgc	atggacccggc	ggggaggac	ctggaagctg	660
ctgggcttg	tggcttatgc	ccacagcaag	gagctggta	ctgcctggta	catcggtt	720
ctttgtctca	tccctggctc	gttcttgg	tacttggcag	agaaggggg	gaacgaccac	780
tttgacacct	acgcggatgc	actctggtgg	ggcctgatca	cgctgaccac	cattggctac	840
ggggacaact	accccccagac	ctggAACGGC	aggctcctt	cggaacac	caccctcatc	900
ggtgtctct	tcttcgcgt	gcctgcaggc	atcttgggtt	ctgggttgc	cctgaaggtt	960
caggagcagc	acaggcagaa	gcacttttag	aaagaggcgg	acccggcagc	aggcctgatc	1020
cagtccgcct	ggagattcta	cgccaccaac	ctctcgcgc	cagacctgca	ctccacgtgg	1080
cagtactacg	agcgaacgg	caccgtgccc	atgtacagtt	cgcaactca	aacctacggg	1140
gcctccagac	ttatcccccc	gctgaaccag	ctggagctgc	tgaggaacct	caagagtaaa	1200
tctggactcg	cttcaggaa	ggacccccc	ccggagccgt	ctccaagcca	gaaggtcaagt	1260
ttgaaagatc	gtgtcttctc	cagccccg	ggcgtggctg	ccaaggggg	gggtccccg	1320
caggcccaga	ctgtgaggcg	gtcacc	ggcggaccaga	gcctcgagga	cagccccagc	1380
aagggtgcca	agagctggag	cttcggggac	cgcagccggg	cacggcaggc	tttccgcata	1440
aagggtggcg	cgtcacggc	gaactcaaaa	aaagcaagcc	tcccccggaga	ggacattgtg	1500
gatgacaaga	gctccccctg	cgagttgt	accgaggacc	tgacccggg	cctcaaagtc	1560
agcatcagag	ccgtgtgt	catgcgg	ctgtgttca	agcgaagtt	caaggagac	1620
ctggggccct	acagcgtgtat	ggacgtcata	gagcgtact	cagccggca	cctggacatg	1680
ctgtcccga	ttaagagcct	gcagtccaga	gtggaccaga	tcgtggggcg	ggggccagcg	1740
atcacggaca	aggacggcac	caagggccc	ggcgaggccg	agctgcccga	ggaccccagc	1800
atgatgggac	ggctcgggaa	ggtggagaag	caggctt	ccatggagaa	gaagctggac	1860
ttcctggtga	atatctacat	gcagcgat	ggcatcccc	cgacagagac	cgaggcctac	1920
tttggggcca	aagagccgga	gccggcccg	ccgttaccaca	gccccggaa	cagccggag	1980
catgtcgaca	ggcacggctg	cattgtcaag	atcgtgcgt	ccagcagctc	cacggggccag	2040
aagaacttct	cgccgc	ggccgcgc	cctgtccagt	gtccgcctc	cacctccctgg	2100
cagccacaga	gccacc	ccagg	ggcac	ccgtgggg	ccacggctcc	2160
ctggtgcc	tccgc	gcctgccc	gagcgg	tcata	cgccggggc	2220
aaccgcgca	gcatgg	cctgcgg	gaggac	ccgg	ggcccccggag	2280
gggaccctgc	gggacagcga	cacgtccatc	tccatccc	ccgtggacca	cgaggagctg	2340
gagcgttct	tcagcggctt	cagcat	cagtccaa	agaac	tgctctcaac	2400
agctgctacg	cggccgtggc	gcctt	aaagt	cag	ggagggagag	2460
tcagacaccg	actccgac	ctgtac	ccat	cc	ggccacccggc	2520
gagggtccct	ttgg	gacgt	ggc	ggccc	agtga	2565

<210> 3  
<211> 854  
<212> PRT  
<213> Homo sapiens

<400> 3

Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly  
1 5 10 15  
Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro  
20 25 30  
Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro  
35 40 45  
Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala  
50 55 60  
Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe  
65 70 75 80  
Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His  
85 90 95  
Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe  
100 105 110  
Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile  
115 120 125  
Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg  
130 135 140  
Ile Trp Ala Ala Gly Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg  
145 150 155 160  
Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu  
165 170 175  
Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe  
180 185 190  
Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met  
195 200 205  
Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Gly Ser Val  
210 215 220  
Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe  
225 230 235 240  
Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly  
245 250 255  
Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu  
260 265 270  
Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp  
275 280 285  
Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe  
290 295 300  
Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val  
305 310 315 320  
Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala  
325 330 335  
Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser  
340 345 350  
Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr  
355 360 365  
Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu  
370 375 380  
Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys  
385 390 395 400  
Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser  
405 410 415  
Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg Gly Val  
420 425 430  
Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg Arg Ser  
435 440 445  
Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val Pro Lys  
450 455 460  
Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe Arg Ile  
465 470 475 480  
Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu Pro Gly  
485 490 495  
Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val Thr Glu  
500 505 510  
Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys Val Met

515	520	525
Arg Phe Leu Val Ser Lys Arg	Lys Phe Lys Glu Ser	Leu Arg Pro Tyr
530	535	540
Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His	Leu Asp Met	
545	550	555 560
Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Val Asp Gln	Ile Val Gly	
565	570	575
Arg Gly Pro Ala Ile Thr Asp Lys Asp Arg Thr Lys Gly	Pro Ala Glu	
580	585	590
Ala Glu Leu Pro Glu Asp Pro Ser Met Met Gly Arg	Leu Gly Lys Val	
595	600	605
Glu Lys Gln Val Leu Ser Met Glu Lys Lys Leu Asp Phe	Leu Val Asn	
610	615	620
Ile Tyr Met Gln Arg Met Gly Ile Pro Pro Thr Glu Thr	Glu Ala Tyr	
625	630	635 640
Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro Pro Tyr His	Ser Pro Glu	
645	650	655
Asp Ser Arg Glu His Val Asp Arg His Gly Cys Ile Val	Lys Ile Val	
660	665	670
Arg Ser Ser Ser Thr Gly Gln Lys Asn Phe Ser Ala Pro	Pro Ala	
675	680	685
Ala Pro Pro Val Gln Cys Pro Pro Ser Thr Ser Trp Gln	Pro Gln Ser	
690	695	700
His Pro Arg Gln Gly His Gly Thr Ser Pro Val Gly Asp	His Gly Ser	
705	710	715 720
Leu Val Arg Ile Pro Pro Pro Ala His Glu Arg Ser Leu	Ser Ala	
725	730	735
Tyr Gly Gly Asn Arg Ala Ser Met Glu Phe Leu Arg Gln	Glu Asp	
740	745	750
Thr Pro Gly Cys Arg Pro Pro Glu Gly Thr Leu Arg Asp	Ser Asp Thr	
755	760	765
Ser Ile Ser Ile Pro Ser Val Asp His Glu Glu Leu Glu	Arg Ser Phe	
770	775	780
Ser Gly Phe Ser Ile Ser Gln Ser Lys Glu Asn Leu Asp	Ala Leu Asn	
785	790	795 800
Ser Cys Tyr Ala Ala Val Ala Pro Cys Ala Lys Val Arg	Pro Tyr Ile	
805	810	815
Ala Glu Gly Glu Ser Asp Thr Asp Ser Asp Leu Cys Thr	Pro Cys Gly	
820	825	830
Pro Pro Pro Arg Ser Ala Thr Gly Glu Gly Pro Phe	Gly Asp Val Gly	
835	840	845
Trp Ala Gly Pro Arg Lys		
850		

<210> 4

<211> 1425

<212> DNA

<213> Homo sapiens

<400> 4

cgccggagcga	ggtgtggccgca	gcgtctccgc	gcccggccca	agcccgccag	gagtgcggaa	60
ccggccgcctc	ggccatgcgg	ctccccggccg	ggggggctgg	gctggggccc	gcgcgcgc	120
ccgcgcgtccg	cccccgctga	gcctgagccc	gaccggggc	gcctcccgcc	aggcaccatg	180
gtcagaagt	cgcgaacgg	cggcgatac	cccgccccg	gcggggagaa	gaagctgaag	240
gtgggcttcg	tggggcttgg	ccccggcg	cccgactcca	cccgggacgg	ggcgctgtcg	300
atcgccggct	ccgaggcccc	caagcgccgc	agcatcctca	gcaaacctcg	cgcgggccc	360
gcggggcccg	ggaagccccc	caagcgcaac	gccttctacc	gcaagctgca	aatattcctc	420
tacaacgtgc	tggagcggcc	gcccggctgg	gcgttcatct	accacgccta	cgtgttctc	480
ctggttttct	cctgcctcg	gtgtctgt	tttccacca	tcaaggat	tgagaagagc	540
tcggaggggg	ccctctacat	cctggaaatc	gtgactatcg	tgggtttgg	cgtggagatc	600
ttcgtgcgga	tctggggccgc	aggctgtgc	tgccgggtacc	gtgggtggag	ggggcggctc	660
aagtttggcc	ggaaacgg	ctgtgtgatt	gacatcatgg	tgctcatecg	ctccattgc	720
gtgctggccg	ccgcgtccca	ggcaacgtc	tttgcacat	ctgcgtccg	gaggcctgcgc	780
ttcctgcaga	ttctgcggat	gatccgcatg	gaccggcggg	gaggcacctg	gaagctgtcg	840
ggctctgtgg	tctatgccc	cagcaaggag	ctggtaactg	cctggtaat	cggcttcctt	900
tgtctcatcc	ttggctcg	cctgggtac	ttggcagaga	agggggagaa	cgaccactt	960

gacacctacg	cggatgcact	ctgggtggggc	ctgatcacgc	tgaccaccat	tggctacggg	1020
gacaagtacc	cccgacacctg	gaacggcagg	ctccttgcgg	caaccttcac	cctcatcggt	1080
gtctcccttct	tcgcgtgcc	tgcaggcatac	ttggggctcg	ggtttgcct	gaaggttcag	1140
gaggcagcaca	ggcagaagca	ctttgagaag	aggcggaaacc	cggcagcagg	cctgatccag	1200
tcggccttgg	gattctacgc	caccaacctc	tcgcgcacag	acctgcactc	cacgtggcag	1260
tactacgagc	gaacggtac	cgtgccccatg	tacaggtacc	gccggccgggc	acctgcccacc	1320
aagcaactgt	ttcatttttt	attttccatt	tgttcttaaa	ccccactttt	tgttgttcat	1380
tatTTTgatt	gatttttttt	ctttaaaaatg	tatTTTcac	aaagg		1425

<210> 5  
<211> 393  
<212> PRT  
<213> *Homo sapiens*

<400> 5  
 Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly  
 1 5 10 15  
 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro  
 20 25 30  
 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro  
 35 40 45  
 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala  
 50 55 60  
 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe  
 65 70 75 80  
 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His  
 85 90 95  
 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe  
 100 105 110  
 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile  
 115 120 125  
 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg  
 130 135 140  
 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg  
 145 150 155 160  
 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu  
 165 170 175  
 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe  
 180 185 190  
 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met  
 195 200 205  
 Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val  
 210 215 220  
 Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe  
 225 230 235 240  
 Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly  
 245 250 255  
 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu  
 260 265 270  
 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp  
 275 280 285  
 Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe  
 290 295 300  
 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val  
 305 310 315 320  
 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala  
 325 330 335  
 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser  
 340 345 350  
 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr  
 355 360 365  
 Val Pro Met Tyr Arg Tyr Arg Arg Arg Ala Pro Ala Thr Lys Gln Leu  
 370 375 380  
 Phe His Phe Leu Phe Ser Ile Cys Ser.  
 385 390

<210> 6  
<211> 581  
<212> PRT  
<213> Homo sapiens

<400> 6  
Met Glu Thr Arg Gly Ser Arg Leu Thr Gly Gly Gln Gly Arg Val Tyr  
1 5 10 15  
Asn Phe Leu Glu Arg Pro Thr Gly Trp Lys Cys Phe Val Tyr His Phe  
20 25 30  
Ala Val Phe Leu Ile Val Leu Val Cys Leu Ile Phe Ser Val Leu Ser  
35 40 45  
Thr Ile Glu Gln Tyr Ala Ala Thr Gly Thr Leu Phe Trp Met  
50 55 60  
Glu Ile Val Leu Val Val Phe Phe Gly Thr Glu Tyr Val Val Arg Leu  
65 70 75 80  
Trp Ser Ala Gly Cys Arg Ser Lys Tyr Val Gly Leu Trp Gly Arg Leu  
85 90 95  
Arg Phe Ala Arg Lys Pro Ile Ser Ile Ile Asp Leu Ile Val Val Val  
100 105 110  
Ala Ser Met Val Val Leu Cys Val Gly Ser Lys Gly Gln Val Phe Ala  
115 120 125  
Thr Ser Ala Ile Arg Gly Ile Arg Phe Leu Gln Ile Leu Arg Met Leu  
130 135 140  
His Val Asp Arg Gln Gly Gly Thr Trp Arg Leu Leu Gly Ser Val Val  
145 150 155 160  
Phe Ile His Arg Gln Glu Leu Ile Thr Thr Leu Tyr Ile Gly Phe Leu  
165 170 175  
Gly Leu Ile Phe Ser Ser Tyr Phe Val Tyr Leu Ala Glu Lys Asp Ala  
180 185 190  
Val Asn Glu Ser Gly Arg Val Glu Phe Gly Ser Tyr Ala Asp Ala Leu  
195 200 205  
Trp Trp Gly Val Val Thr Val Thr Thr Ile Gly Tyr Gly Asp Lys Val  
210 215 220  
Pro Gln Thr Trp Val Gly Lys Thr Ile Ala Ser Cys Phe Ser Val Phe  
225 230 235 240  
Ala Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe  
245 250 255  
Ala Leu Lys Val Gln Gln Lys Gln Arg Gln Lys His Phe Asn Arg Gln  
260 265 270  
Ile Pro Ala Ala Ala Ser Leu Ile Gln Thr Ala Trp Arg Cys Tyr Ala  
275 280 285  
Ala Glu Asn Pro Asp Ser Ser Thr Trp Lys Ile Tyr Ile Arg Lys Ala  
290 295 300  
Pro Arg Ser His Thr Leu Leu Ser Pro Ser Pro Lys Pro Lys Lys Ser  
305 310 315 320  
Val Val Val Lys Lys Lys Phe Lys Leu Asp Lys Asp Asn Gly Val  
325 330 335  
Thr Pro Gly Glu Lys Met Leu Thr Val Pro His Ile Thr Cys Asp Pro  
340 345 350  
Pro Glu Glu Arg Arg Leu Asp His Phe Ser Val Asp Gly Tyr Asp Ser  
355 360 365  
Ser Val Arg Lys Ser Pro Thr Leu Leu Glu Val Ser Met Pro His Phe  
370 375 380  
Met Arg Thr Asn Ser Phe Ala Glu Asp Leu Asp Leu Glu Gly Glu Thr  
385 390 395 400  
Leu Leu Thr Pro Ile Thr His Ile Ser Gln Leu Arg Glu His His Arg  
405 410 415  
Ala Thr Ile Lys Val Ile Arg Arg Met Gln Tyr Phe Val Ala Lys Lys  
420 425 430  
Lys Phe Gln Gln Ala Arg Lys Pro Tyr Asp Val Arg Asp Val Ile Glu  
435 440 445  
Gln Tyr Ser Gln Gly His Leu Asn Leu Met Val Arg Ile Lys Glu Leu  
450 455 460  
Gln Arg Arg Leu Asp Gln Ser Ile Gly Lys Pro Ser Leu Phe Ile Ser  
465 470 475 480

Val Ser Glu Lys Ser Lys Asp Arg Gly Ser Asn Thr Ile Gly Ala Arg  
485 490 495  
Leu Asn Arg Val Glu Asp Lys Val Thr Gln Leu Asp Gln Arg Leu Ala  
500 505 510  
Leu Ile Thr Asp Met Leu His Gln Leu Leu Ser Leu His Gly Gly Ser  
515 520 525  
Thr Pro Gly Ser Gly Gly Pro Pro Arg Glu Gly Gly Ala His Ile Thr  
530 535 540  
Gln Pro Cys Gly Ser Gly Gly Ser Val Asp Pro Glu Leu Phe Leu Pro  
545 550 555 560  
Ser Asn Thr Leu Pro Thr Tyr Glu Gln Leu Thr Val Pro Arg Arg Gly  
565 570 575  
Pro Asp Glu Gly Ser  
580

<210> 7  
<211> 872  
<212> PRT  
<213> Rattus

<400> 7  
Met Gly Leu Lys Ala Arg Arg Ala Ala Gly Ala Ala Gly Gly Gly  
1 5 10 15  
Gly Glu Gly Gly Gly Gly Gly Ala Ala Asn Pro Ala Gly Gly  
20 25 30  
Asp Ser Ala Val Ala Gly Asp Glu Glu Arg Lys Val Gly Leu Ala Pro  
35 40 45  
Gly Asp Val Glu Gln Val Thr Leu Ala Leu Gly Thr Gly Ala Asp Lys  
50 55 60  
Asp Gly Thr Leu Leu Leu Glu Gly Gly Arg Glu Glu Gly Gln Arg  
65 70 75 80  
Arg Thr Pro Gln Gly Ile Gly Leu Leu Ala Lys Thr Pro Leu Ser Arg  
85 90 95  
Pro Val Lys Arg Asn Asn Ala Lys Tyr Arg Arg Ile Gln Thr Leu Ile  
100 105 110  
Tyr Asp Ala Leu Glu Arg Pro Arg Gly Trp Ala Leu Leu Tyr His Ala  
115 120 125  
Leu Val Phe Leu Ile Val Leu Gly Cys Leu Ile Leu Ala Val Leu Thr  
130 135 140  
Thr Phe Lys Glu Tyr Glu Thr Val Ser Gly Asp Trp Leu Leu Val Pro  
145 150 155 160  
Glu Thr Phe Ala Ile Phe Ile Phe Gly Ala Glu Phe Ala Leu Arg Ile  
165 170 175  
Trp Ala Ala Gly Cys Cys Cys Arg Tyr Lys Gly Trp Arg Gly Arg Leu  
180 185 190  
Lys Phe Ala Arg Lys Pro Leu Cys Met Leu Asp Ile Phe Val Leu Ile  
195 200 205  
Ala Ser Val Pro Val Val Ala Val Gly Asn Gln Gly Asn Val Leu Ala  
210 215 220  
Thr Ser Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met Leu Arg  
225 230 235 240  
Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Ala Ile Cys  
245 250 255  
Ala His Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Thr  
260 265 270  
Leu Ile Leu Ser Ser Phe Leu Val Tyr Leu Val Glu Lys Asp Val Pro  
275 280 285  
Glu Met Asp Ala Gln Gly Glu Glu Met Lys Glu Glu Phe Glu Thr Tyr  
290 295 300  
Ala Asp Ala Leu Trp Trp Gly Leu Ile Thr Leu Ala Thr Ile Gly Tyr  
305 310 315 320  
Gly Asp Lys Thr Pro Lys Thr Trp Glu Gly Arg Leu Ile Ala Ala Thr  
325 330 335  
Phe Ser Leu Ile Gly Val Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu  
340 345 350  
Gly Ser Gly Leu Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His

355	360	365													
Phe	Glu	Lys	Arg	Arg	Lys	Pro	Ala	Ala	Glu	Leu	Ile	Gln	Ala	Ala	Trp
370						375					380				
Arg	Tyr	Tyr	Ala	Thr	Asn	Asn	Arg	Leu	Asp	Leu	Val	Ala	Thr	Trp	Arg
385					390					395					400
Phe	Tyr	Glu	Ser	Val	Val	Ser	Phe	Pro	Phe	Phe	Arg	Lys	Glu	Gln	Leu
					405				410						415
Glu	Ala	Ala	Ala	Ser	Gln	Lys	Leu	Gly	Leu	Leu	Asp	Arg	Val	Arg	Leu
					420			425							430
Ser	Asn	Pro	Arg	Gly	Ser	Asn	Thr	Lys	Gly	Lys	Leu	Phe	Thr	Pro	Leu
					435			440							445
Asn	Val	Asp	Ala	Ile	Glu	Glu	Ser	Pro	Ser	Lys	Glu	Pro	Lys	Pro	Val
					450			455							460
Gly	Leu	Asn	Asn	Lys	Glu	Arg	Phe	Arg	Thr	Ala	Phe	Arg	Met	Lys	Ala
465					470				475						480
Tyr	Ala	Phe	Trp	Gln	Ser	Ser	Glu	Asp	Ala	Gly	Thr	Gly	Asp	Pro	Met
					485				490						495
Thr	Glu	Asp	Arg	Gly	Tyr	Gly	Asn	Asp	Phe	Leu	Ile	Glu	Asp	Met	Ile
					500				505						510
Pro	Thr	Leu	Lys	Ala	Ala	Ile	Arg	Ala	Val	Arg	Ile	Leu	Gln	Phe	Arg
					515				520						525
Leu	Tyr	Lys	Lys	Phe	Lys	Glu	Thr	Leu	Arg	Pro	Tyr	Asp	Val	Lys	
					530			535							540
Asp	Val	Ile	Glu	Gln	Tyr	Ser	Ala	Gly	His	Leu	Asp	Met	Leu	Ser	Arg
545					550					555					560
Ile	Lys	Tyr	Leu	Gln	Thr	Arg	Ile	Asp	Met	Ile	Phe	Thr	Pro	Gly	Pro
					565				570						575
Pro	Ser	Thr	Pro	Lys	His	Lys	Ser	Gln	Lys	Gly	Ser	Ala	Phe	Thr	
					580				585						590
Tyr	Pro	Ser	Gln	Gln	Ser	Pro	Arg	Asn	Glu	Pro	Tyr	Val	Ala	Arg	Ala
					595				600						605
Ala	Thr	Ser	Glu	Thr	Glu	Asp	Gln	Ser	Met	Met	Gly	Lys	Phe	Val	Lys
					610			615							620
Val	Glu	Arg	Gln	Val	His	Asp	Met	Gly	Lys	Lys	Leu	Asp	Phe	Leu	Val
					625			630			635				640
Asp	Met	His	Met	Gln	His	Met	Glu	Arg	Leu	Gln	Val	His	Val	Thr	Glu
					645				650						655
Tyr	Tyr	Pro	Thr	Lys	Gly	Ala	Ser	Ser	Pro	Ala	Glu	Gly	Glu	Lys	Lys
					660			665							670
Glu	Asp	Asn	Arg	Tyr	Ser	Asp	Leu	Lys	Thr	Ile	Ile	Cys	Asn	Tyr	Ser
					675			680				685			
Glu	Ser	Gly	Pro	Pro	Asp	Pro	Pro	Tyr	Ser	Phe	His	Gln	Val	Pro	Ile
					690			695							700
Asp	Arg	Val	Gly	Pro	Tyr	Gly	Phe	Phe	Ala	His	Asp	Pro	Val	Lys	Leu
705					710				715						720
Thr	Arg	Gly	Gly	Pro	Ser	Ser	Thr	Lys	Ala	Gln	Ala	Asn	Leu	Pro	Ser
					725				730						735
Ser	Gly	Ser	Thr	Tyr	Ala	Glu	Arg	Pro	Thr	Val	Leu	Pro	Ile	Leu	Thr
					740				745						750
Leu	Leu	Asp	Ser	Cys	Val	Ser	Tyr	His	Ser	Gln	Thr	Glu	Leu	Gln	Gly
					755				760						765
Pro	Tyr	Ser	Asp	His	Ile	Ser	Pro	Arg	Gln	Arg	Arg	Ser	Ile	Thr	Arg
					770			775							780
Asp	Ser	Asp	Thr	Pro	Leu	Ser	Leu	Met	Ser	Val	Asn	His	Glu	Glu	Leu
					785			790							800
Glu	Arg	Ser	Pro	Ser	Gly	Phe	Ser	Ile	Ser	Gln	Asp	Arg	Asp	Asp	Tyr
					805				810						815
Val	Phe	Gly	Pro	Ser	Gly	Gly	Ser	Ser	Trp	Met	Arg	Glu	Lys	Arg	Tyr
					820				825						830
Leu	Ala	Glu	Gly	Glu	Thr	Asp	Thr	Asp	Thr	Asp	Pro	Phe	Thr	Pro	Ser
					835				840						845
Gly	Ser	Met	Pro	Met	Ser	Ser	Thr	Gly	Asp	Gly	Ile	Ser	Asp	Ser	Ile
					850				855						860
Trp	Thr	Pro	Ser	Asn	Lys	Pro	Thr								
					865				870						

<210> 8  
<211> 825  
<212> PRT  
<213> Homo sapiens

<400> 8  
Gly Asp Val Glu Gln Val Thr Leu Ala Leu Gly Ala Gly Ala Asp Lys  
1 5 10 15  
Asp Gly Thr Leu Leu Leu Glu Gly Gly Arg Asp Glu Gly Gln Arg  
20 25 30  
Arg Thr Pro Gln Gly Ile Gly Leu Leu Ala Lys Thr Pro Leu Ser Arg  
35 40 45  
Pro Val Lys Arg Asn Asn Ala Lys Tyr Arg Arg Ile Gln Thr Leu Ile  
50 55 60  
Tyr Asp Ala Leu Glu Arg Pro Arg Gly Trp Ala Leu Leu Tyr His Ala  
65 70 75 80  
Leu Val Phe Leu Ile Val Leu Gly Cys Leu Ile Leu Ala Val Leu Thr  
85 90 95  
Thr Phe Lys Glu Tyr Glu Thr Val Ser Gly Asp Trp Leu Leu Leu  
100 105 110  
Glu Thr Phe Ala Ile Phe Ile Phe Gly Ala Glu Phe Ala Leu Arg Ile  
115 120 125  
Trp Ala Ala Gly Cys Cys Arg Tyr Lys Gly Trp Arg Gly Arg Leu  
130 135 140  
Lys Phe Ala Arg Lys Pro Leu Cys Met Leu Asp Ile Phe Val Leu Ile  
145 150 155 160  
Ala Ser Val Pro Val Val Ala Val Gly Asn Gln Gly Asn Val Leu Ala  
165 170 175  
Thr Ser Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met Leu Arg  
180 185 190  
Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Ala Ile Cys  
195 200 205  
Ala His Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Thr  
210 215 220  
Leu Ile Leu Ser Ser Phe Leu Val Tyr Leu Val Glu Lys Asp Val Pro  
225 230 235 240  
Glu Val Asp Ala Gln Gly Glu Glu Met Lys Glu Glu Phe Glu Thr Tyr  
245 250 255  
Ala Asp Ala Leu Trp Trp Gly Leu Ile Thr Leu Ala Thr Ile Gly Tyr  
260 265 270  
Gly Asp Lys Thr Pro Lys Thr Trp Glu Gly Arg Leu Ile Ala Ala Thr  
275 280 285  
Phe Ser Leu Ile Gly Val Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu  
290 295 300  
Gly Ser Gly Leu Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His  
305 310 315 320  
Phe Glu Lys Arg Arg Lys Pro Ala Ala Glu Leu Ile Gln Ala Ala Trp  
325 330 335  
Arg Tyr Tyr Ala Thr Asn Pro Asn Arg Ile Asp Leu Val Ala Thr Trp  
340 345 350  
Arg Phe Tyr Glu Ser Val Val Ser Phe Pro Phe Phe Arg Lys Glu Gln  
355 360 365  
Leu Glu Ala Ala Ser Ser Gln Lys Leu Gly Leu Leu Asp Arg Val Arg  
370 375 380  
Leu Ser Asn Pro Arg Gly Ser Asn Thr Lys Gly Lys Leu Phe Thr Pro  
385 390 395 400  
Leu Asn Val Asp Ala Ile Glu Glu Ser Pro Ser Lys Glu Pro Lys Pro  
405 410 415  
Val Gly Leu Asn Asn Lys Glu Arg Phe Arg Thr Ala Phe Arg Met Lys  
420 425 430  
Ala Tyr Ala Phe Trp Gln Ser Ser Glu Asp Ala Gly Thr Gly Asp Pro  
435 440 445  
Met Ala Glu Asp Arg Gly Tyr Gly Asn Asp Phe Pro Ile Glu Asp Met  
450 455 460  
Ile Pro Thr Leu Lys Ala Ala Ile Arg Ala Val Arg Ile Leu Gln Phe  
465 470 475 480

Arg Leu Tyr Lys Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val  
           485                  490                  495  
 Lys Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Ser  
           500                  505                  510  
 Arg Ile Lys Tyr Leu Gln Thr Arg Ile Asp Met Ile Phe Thr Pro Gly  
           515                  520                  525  
 Pro Pro Ser Thr Pro Lys His Lys Ser Gln Lys Gly Ser Ala Phe  
           530                  535                  540  
 Thr Phe Pro Ser Gln Gln Ser Pro Arg Asn Glu Pro Tyr Val Ala Arg  
           545                  550                  555                  560  
 Pro Ser Thr Ser Glu Ile Glu Asp Gln Ser Met Met Gly Lys Phe Val  
           565                  570                  575  
 Lys Val Glu Arg Gln Val Gln Asp Met Gly Lys Lys Leu Asp Phe Leu  
           580                  585                  590  
 Val Asp Met His Met Gln His Met Glu Arg Leu Gln Val Gln Val Thr  
           595                  600                  605  
 Glu Tyr Tyr Pro Thr Lys Gly Thr Ser Ser Pro Ala Glu Ala Glu Lys  
           610                  615                  620  
 Lys Glu Asp Asn Arg Tyr Ser Asp Leu Lys Thr Ile Ile Cys Asn Tyr  
           625                  630                  635                  640  
 Ser Glu Thr Gly Pro Pro Glu Pro Pro Tyr Ser Phe His Gln Val Thr  
           645                  650                  655  
 Ile Asp Lys Val Ser Pro Tyr Gly Phe Phe Ala His Asp Pro Val Asn  
           660                  665                  670  
 Leu Pro Arg Gly Gly Pro Ser Ser Gly Lys Val Gln Ala Thr Pro Pro  
           675                  680                  685  
 Ser Ser Ala Thr Thr Tyr Val Glu Arg Pro Thr Val Leu Pro Ile Leu  
           690                  695                  700  
 Thr Leu Leu Asp Ser Arg Val Ser Cys His Ser Gln Ala Asp Leu Gln  
           705                  710                  715                  720  
 Gly Pro Tyr Ser Asp Arg Ile Ser Pro Arg Gln Arg Arg Ser Ile Thr  
           725                  730                  735  
 Arg Asp Ser Asp Thr Pro Leu Ser Leu Met Ser Val Asn His Glu Glu  
           740                  745                  750  
 Leu Glu Arg Ser Pro Ser Gly Phe Ser Ile Ser Gln Asp Arg Asp Asp  
           755                  760                  765  
 Tyr Val Phe Gly Pro Asn Gly Gly Ser Ser Trp Met Arg Glu Lys Arg  
           770                  775                  780  
 Tyr Leu Ala Glu Gly Glu Thr Asp Thr Asp Thr Asp Pro Phe Thr Pro  
           785                  790                  795                  800  
 Ser Gly Ser Met Pro Leu Ser Ser Thr Gly Asp Gly Ile Ser Asp Ser  
           805                  810                  815  
 Val Trp Thr Pro Ser Asn Lys Pro Ile  
           820                  825

<210> 9  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 9

aacctctcgc gcacagaccc gca

23

<210> 10  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 10

aacagtgtgct tgggtggcagg agcc

24